

SEQUENCE LISTING

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Hall, Heike

<120> ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING

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<150> 10/024,918  
<151> 2001-12-18

<150> 09/057,052  
<151> 1998-04-08

<150> PCT/US98/06617  
<151> 1998-04-02

<150> 60/042,143  
<151> 1997-04-03

<160> 33

<170> PatentIn version 3.1

<210> 1  
<211> 5  
<212> PRT  
<213> artificial sequence

<220>  
<223> receptor-binding domain of laminin B1 chain

<400> 1

Tyr Ile Gly Ser Arg  
1 5

<210> 2  
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<212> PRT  
<213> artificial sequence

<220>  
<223> receptor-binding domain of laminin A chain

<400> 2

Leu Arg Gly Asp Asn  
1 5

<210> 3  
<211> 5

<212> PRT  
<213> artificial sequence

<220>  
<223> receptor-binding domain of laminin B1 chain

<400> 3

Pro Asp Gly Ser Arg  
1 5

<210> 4  
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<212> PRT  
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<220>  
<223> recognition sequence of the laminin A chain

<400> 4

Ile Lys Val Ala Val  
1 5

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<212> PRT  
<213> artificial sequence

<220>  
<223> recognition sequence of the laminin B2 chain

<400> 5

Arg Asn Ile Ala Glu Ile Ile Lys Asp Ile  
1 5 10

<210> 6  
<211> 4  
<212> PRT  
<213> artificial sequence

<220>  
<223> collagen peptide that binds to the alpha 2 beta 1 integrin

<400> 6

Asp Gly Glu Ala  
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<210> 7  
<211> 6  
<212> PRT

<213> artificial sequence

<220>

<223> heparin-binding sequence from fibronectin

<400> 7

Pro Arg Arg Ala Arg Val  
1 5

<210> 8

<211> 16

<212> PRT

<213> artificial sequence

<220>

<223> peptide with glutamine at the transglutaminase coupling site and  
an active peptide that mimics the crosslinking site in the gamma  
chain of fibrinogen

<220>

<221> MOD\_RES

<222> (1)..(1)

<223> dansylated tyrosine

<400> 8

Tyr Arg Gly Asp Thr Ile Gly Glu Gly Gln Gln His His Leu Gly Gly  
1 5 10 15

<210> 9

<211> 9

<212> PRT

<213> artificial sequence

<220>

<223> peptide that mimics the lysine coupling site in the gamma chain o  
f fibrinogen with an active peptide sequence

<220>

<221> MOD\_RES

<222> (1)..(1)

<223> dansylated leucine

<400> 9

Leu Arg Gly Asp Gly Ala Lys Asp Val  
1 5

<210> 10

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> random coupling polylysine peptide attached to active peptide

<220>

<221> MOD\_RES

<222> (1)..(1)

<223> dansylated leucine

<400> 10

Leu Arg Gly Lys Lys Lys Lys Gly

1

5

<210> 11

<211> 12

<212> PRT

<213> artificial sequence

<220>

<223> peptide that mimics the crosslinking site in alpha 2- plasmin inhibitor with an active peptide sequence

<220>

<221> MOD\_RES

<222> (1)..(1)

<223> dansylated leucine

<400> 11

Leu Asn Gln Glu Gln Val Ser Pro Leu Arg Gly Asp

1

5

10

<210> 12

<211> 16

<212> PRT

<213> artificial sequence

<220>

<223> peptide with glutamine at the transglutaminase coupling site in the chain of fibrinogen

<400> 12

Tyr Arg Gly Asp Thr Ile Gly Glu Gly Gln Gln His His Leu Gly Gly

1

5

10

15

<210> 13

<211> 5

<212> PRT

<213> artificial sequence

<220>  
<223> peptide that mimics the lysine coupling site in the chain of fibrinogen

<400> 13

Gly Ala Lys Asp Val  
1 5

<210> 14  
<211> 4  
<212> PRT  
<213> artificial sequence

<220>  
<223> peptide with a polylysine at a random coupling site

<400> 14

Lys Lys Lys Lys  
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<210> 15  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<223> peptide that mimics the crosslinking site in alpha 2- plasmin inhibitor ( abbreviated TG)

<400> 15

Asn Gln Glu Gln Val Ser Pro Leu  
1 5

<210> 16  
<211> 15  
<212> PRT  
<213> artificial sequence

<220>  
<223> peptide that mimics the crosslinking site in alpha 2- plasmin inhibitor with active peptide sequence

<220>  
<221> MOD\_RES  
<222> (1)..(1)  
<223> dansylated leucine

<400> 16

Leu Asn Gln Glu Gln Val Ser Pro Leu Gly Tyr Ile Gly Ser Arg  
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<220>  
<223> peptide that mimics the crosslinking site in alpha 2- plasmin inh  
ibitor with active peptide sequence

<220>  
<221> MOD\_RES  
<222> (1)..(1)  
<223> dansylated leucine

<400> 17

Leu Asn Gln Glu Gln Val Ser Pro Leu Asp Asp Gly Glu Ala Gly  
1                      5                      10                      15

<210> 18  
<211> 16  
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<213> artificial sequence

<220>  
<223> peptide that mimics the crosslinking site in alpha 2- plasmin inh  
ibitor with active peptide sequence

<220>  
<221> MOD\_RES  
<222> (1)..(1)  
<223> dansylated leucine

<400> 18

Leu Asn Gln Glu Gln Val Ser Pro Leu Arg Ala His Ala Val Ser Glu  
1                      5                      10                      15

<210> 19  
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<213> artificial sequence

<220>  
<223> peptide that mimics the crosslinking site in alpha 2- plasmin inh  
ibitor with active peptide sequence

<220>  
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<222> (1)..(1)  
<223> dansylated leucine

<400> 19

Leu Asn Gln Glu Gln Val Ser Pro Arg Asp Ile Lys Val Ala Val Asp  
1 5 10 15

Gly

<210> 20  
<211> 19  
<212> PRT  
<213> artificial sequence

<220>  
<223> peptide that mimics the crosslinking site in alpha 2- plasmin inh  
ibitor with active peptide sequence

<220>  
<221> MOD\_RES  
<222> (1)..(1)  
<223> dansylated leucine

<400> 20

Leu Asn Gln Glu Gln Val Ser Pro Arg Asn Ile Ala Glu Ile Ile Lys  
1 5 10 15

Asp Ile Arg

<210> 21  
<211> 54  
<212> DNA  
<213> Homo sapien

<400> 21  
cgcggatcca atcaagaaca agtcagtccc cttgcaccca tggcagaagg agga 54

<210> 22  
<211> 35  
<212> DNA  
<213> Homo sapien

<400> 22  
ggaattcctc accgcctcgg cttgtcacaa ttttc 35

<210> 23  
<211> 6  
<212> PRT  
<213> artificial sequence

<220>  
<223> thrombin cleavage site

<400> 23

Gly Leu Val Pro Arg Gly  
1 5

<210> 24  
<211> 26  
<212> DNA  
<213> artificial sequence

<220>  
<223> 1S DNA primer

<400> 24  
cccggatccc gcagcgcaat tgagaa

26

<210> 25  
<211> 35  
<212> DNA  
<213> artificial sequence

<220>  
<223> 2AS DNA primer

<400> 25  
cccgaattct tattactgtg ccctgctctc caacc

35

<210> 26  
<211> 54  
<212> DNA  
<213> artificial sequence

<220>  
<223> 3S DNA primer

<400> 26  
cccggatcca atcaggaaca ggtttctcct ttggaagcaa cccagatcac acag

54

<210> 27  
<211> 1260  
<212> PRT  
<213> Mus Musculus

<220>  
<221> MISC\_FEATURE



<222> (516)..(604)  
<223> the sixth Ig-like domain of the cell adhesion molecule L1

<400> 27

Met Val Val Met Leu Arg Tyr Val Trp Pro Leu Leu Leu Cys Ser Pro  
1 5 10 15

Cys Leu Leu Ile Gln Ile Pro Asp Glu Tyr Lys Gly His His Val Leu  
20 25 30

Glu Pro Pro Val Ile Thr Glu Gln Ser Pro Arg Arg Leu Val Val Phe  
35 40 45

Pro Thr Asp Asp Ile Ser Leu Lys Cys Glu Ala Arg Gly Arg Pro Gln  
50 55 60

Val Glu Phe Arg Trp Thr Lys Asp Gly Ile His Phe Lys Pro Lys Glu  
65 70 75 80

Glu Leu Gly Val Val Val His Glu Ala Pro Tyr Ser Gly Ser Phe Thr  
85 90 95

Ile Glu Gly Asn Asn Ser Phe Ala Gln Arg Phe Gln Gly Ile Tyr Arg  
100 105 110

Cys Tyr Ala Ser Asn Lys Leu Gly Thr Ala Met Ser His Glu Ile Gln  
115 120 125

Leu Val Ala Glu Gly Ala Pro Lys Trp Pro Lys Glu Thr Val Lys Pro  
130 135 140

Val Glu Val Glu Glu Gly Glu Ser Val Val Leu Pro Cys Asn Pro Pro  
145 150 155 160

Pro Ser Ala Ala Pro Pro Arg Ile Tyr Trp Met Asn Ser Lys Ile Phe  
165 170 175

Asp Ile Lys Gln Asp Glu Arg Val Ser Met Gly Gln Asn Gly Asp Leu  
180 185 190

Tyr Phe Ala Asn Val Leu Thr Ser Asp Asn His Ser Asp Tyr Ile Cys  
195 200 205

Asn Ala His Phe Pro Gly Thr Arg Thr Ile Ile Gln Lys Glu Pro Ile  
210 215 220

Asp Leu Arg Val Lys Pro Thr Asn Ser Met Ile Asp Arg Lys Pro Arg  
225 230 235 240

Leu Leu Phe Pro Thr Asn Ser Ser Ser Arg Leu Val Ala Leu Gln Gly  
245 250 255

Gln Ser Leu Ile Leu Glu Cys Ile Ala Glu Gly Phe Pro Thr Pro Thr  
260 265 270

Ile Lys Trp Leu His Pro Ser Asp Pro Met Pro Thr Asp Arg Val Ile  
275 280 285

Tyr Gln Asn His Asn Lys Thr Leu Gln Leu Leu Asn Val Gly Glu Glu  
290 295 300

Asp Asp Gly Glu Tyr Thr Cys Leu Ala Glu Asn Ser Leu Gly Ser Ala  
305 310 315 320

Arg His Ala Tyr Tyr Val Thr Val Glu Ala Ala Pro Tyr Trp Leu Gln  
325 330 335

Lys Pro Gln Ser His Leu Tyr Gly Pro Gly Glu Thr Ala Arg Leu Asp  
340 345 350

Cys Gln Val Gln Gly Arg Pro Gln Pro Glu Ile Thr Trp Arg Ile Asn  
355 360 365

Gly Met Ser Met Glu Thr Val Asn Lys Asp Gln Lys Tyr Arg Ile Glu  
370 375 380

Gln Gly Ser Leu Ile Leu Ser Asn Val Gln Pro Thr Asp Thr Met Val  
385 390 395 400

Thr Gln Cys Glu Ala Arg Asn Gln His Gly Leu Leu Leu Ala Asn Ala  
405 410 415

Tyr Ile Tyr Val Val Gln Leu Pro Ala Arg Ile Leu Thr Lys Asp Asn  
420 425 430

Gln Thr Tyr Met Ala Val Glu Gly Ser Thr Ala Tyr Leu Leu Cys Lys  
435 440 445

Ala Phe Gly Ala Pro Val Pro Ser Val Gln Trp Leu Asp Glu Glu Gly  
450 455 460

Thr Thr Val Leu Gln Asp Glu Arg Phe Phe Pro Tyr Ala Asn Gly Thr  
465 470 475 480

Leu Ser Ile Arg Asp Leu Gln Ala Asn Asp Thr Gly Arg Tyr Phe Cys  
485 490 495

Gln Ala Ala Asn Asp Gln Asn Asn Val Thr Ile Leu Ala Asn Leu Gln  
500 505 510

Val Lys Glu Ala Thr Gln Ile Thr Gln Gly Pro Arg Ser Ala Ile Glu  
515 520 525

Lys Lys Gly Ala Arg Val Thr Phe Thr Cys Gln Ala Ser Phe Asp Pro  
530 535 540

Ser Leu Gln Ala Ser Ile Thr Trp Arg Gly Asp Gly Arg Asp Leu Gln  
545 550 555 560

Glu Arg Gly Asp Ser Asp Lys Tyr Phe Ile Glu Asp Gly Lys Leu Val  
565 570 575

Ile Gln Ser Leu Asp Tyr Ser Asp Gln Gly Asn Tyr Ser Cys Val Ala  
580 585 590

Ser Thr Glu Leu Asp Glu Val Glu Ser Arg Ala Gln Leu Leu Val Val  
595 600 605

Gly Ser Pro Gly Pro Val Pro His Leu Glu Leu Ser Asp Arg His Leu  
610 615 620

Leu Lys Gln Ser Gln Val His Leu Ser Trp Ser Pro Ala Glu Asp His  
625 630 635 640

Asn Ser Pro Ile Glu Lys Tyr Asp Ile Glu Phe Glu Asp Lys Glu Met  
645 650 655

Ala Pro Glu Lys Trp Phe Ser Leu Gly Lys Val Pro Gly Asn Gln Thr

660

665

670

Ser Thr Thr Leu Lys Leu Ser Pro Tyr Val His Tyr Thr Phe Arg Val  
 675 680 685

Thr Ala Ile Asn Lys Tyr Gly Pro Gly Glu Pro Ser Pro Val Ser Glu  
 690 695 700

Ser Val Val Thr Pro Glu Ala Ala Pro Glu Lys Asn Pro Val Asp Val  
 705 710 715 720

Arg Gly Glu Gly Asn Glu Thr Asn Asn Met Val Ile Thr Trp Lys Pro  
 725 730 735

Leu Arg Trp Met Asp Trp Asn Ala Pro Gln Ile Gln Tyr Arg Val Gln  
 740 745 750

Trp Arg Pro Gln Gly Lys Gln Glu Thr Trp Arg Lys Gln Thr Val Ser  
 755 760 765

Asp Pro Phe Leu Val Val Ser Asn Thr Ser Thr Phe Val Pro Tyr Glu  
 770 775 780

Ile Lys Val Gln Ala Val Asn Asn Gln Gly Lys Gly Pro Glu Pro Gln  
 785 790 795 800

Val Thr Ile Gly Tyr Ser Gly Glu Asp Tyr Pro Gln Val Ser Pro Glu  
 805 810 815

Leu Glu Asp Ile Thr Ile Phe Asn Ser Ser Thr Val Leu Val Arg Trp  
 820 825 830

Arg Pro Val Asp Leu Ala Gln Val Lys Gly His Leu Lys Gly Tyr Asn  
 835 840 845

Val Thr Tyr Trp Trp Lys Gly Ser Gln Arg Lys His Ser Lys Arg His  
 850 855 860

Ile His Lys Ser His Ile Val Val Pro Ala Asn Thr Thr Ser Ala Ile  
 865 870 875 880

Leu Ser Gly Leu Arg Pro Tyr Ser Ser Tyr His Val Glu Val Gln Ala  
 885 890 895

Phe Asn Gly Arg Gly Leu Gly Pro Ala Ser Glu Trp Thr Phe Ser Thr  
900 905 910

Pro Glu Gly Val Pro Gly His Pro Glu Ala Leu His Leu Glu Cys Gln  
915 920 925

Ser Asp Thr Ser Leu Leu Leu His Trp Gln Pro Pro Leu Ser His Asn  
930 935 940

Gly Val Leu Thr Gly Tyr Leu Leu Ser Tyr His Pro Val Glu Gly Glu  
945 950 955 960

Ser Lys Glu Gln Leu Phe Phe Asn Leu Ser Asp Pro Glu Leu Arg Thr  
965 970 975

His Asn Leu Thr Asn Leu Asn Pro Asp Leu Gln Tyr Arg Phe Gln Leu  
980 985 990

Gln Ala Thr Thr Gln Gln Gly Gly Pro Gly Glu Ala Ile Val Arg Glu  
995 1000 1005

Gly Gly Thr Met Ala Leu Phe Gly Lys Pro Asp Phe Gly Asn Ile  
1010 1015 1020

Ser Ala Thr Ala Gly Glu Asn Tyr Ser Val Val Ser Trp Val Pro  
1025 1030 1035

Arg Lys Gly Gln Cys Asn Phe Arg Phe His Ile Leu Phe Lys Ala  
1040 1045 1050

Leu Pro Glu Gly Lys Val Ser Pro Asp His Gln Pro Gln Pro Gln  
1055 1060 1065

Tyr Val Ser Tyr Asn Gln Ser Ser Tyr Thr Gln Trp Asn Leu Gln  
1070 1075 1080

Pro Asp Thr Lys Tyr Glu Ile His Leu Ile Lys Glu Lys Val Leu  
1085 1090 1095

Leu His His Leu Asp Val Lys Thr Asn Gly Thr Gly Pro Val Arg  
1100 1105 1110

Val Ser Thr Thr Gly Ser Phe Ala Ser Glu Gly Trp Phe Ile Ala  
 1115 1120 1125

Phe Val Ser Ala Ile Ile Leu Leu Leu Leu Ile Leu Leu Ile Leu  
 1130 1135 1140

Cys Phe Ile Lys Arg Ser Lys Gly Gly Lys Tyr Ser Val Lys Asp  
 1145 1150 1155

Lys Glu Asp Thr Gln Val Asp Ser Glu Ala Arg Pro Met Lys Asp  
 1160 1165 1170

Glu Thr Phe Gly Glu Tyr Arg Ser Leu Glu Ser Asp Asn Glu Glu  
 1175 1180 1185

Lys Ala Phe Gly Ser Ser Gln Pro Ser Leu Asn Gly Asp Ile Lys  
 1190 1195 1200

Pro Leu Gly Ser Asp Asp Ser Leu Ala Asp Tyr Gly Gly Ser Val  
 1205 1210 1215

Asp Val Gln Phe Asn Glu Asp Gly Ser Phe Ile Gly Gln Tyr Ser  
 1220 1225 1230

Gly Lys Lys Glu Lys Glu Ala Ala Gly Gly Asn Asp Ser Ser Gly  
 1235 1240 1245

Ala Thr Ser Pro Ile Asn Pro Ala Val Ala Leu Glu  
 1250 1255 1260

<210> 28

<211> 42

<212> PRT

<213> artificial sequence

<220>

<223> peptide, TGPTH, synthesized using a Factor XIIIa substrate sequence (TG) and the first 34 amino acids of the parathyroid hormone (PTH)

<400> 28

Asn Gln Glu Gln Val Ser Pro Leu Ser Val Ser Glu Ile Gln Leu Met  
 1 5 10 15

His Asn Leu Gly Lys His Leu Asn Ser Met Glu Arg Val Glu Trp Leu  
 20 25 30

Arg Lys Lys Leu Gln Asp Val His Asn Phe  
 35 40

<210> 29  
 <211> 51  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> a sense DNA primer

<400> 29  
 cgcggatcca atcaagaaca agtcagtccc cttaagtcca tcgttttaga c 51

<210> 30  
 <211> 44  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> an antisense DNA primer

<400> 30  
 agtcacgatg cggccgcgca gcattctgaa cccagtatac tgga 44

<210> 31  
 <211> 34  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> a sense DNA primer encoding part of the Factor XIIIa substrate and a custom NdeI site

<400> 31  
 ggaattccat atgaatcaag aacaagtcag tccc 34

<210> 32  
 <211> 30  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> an antisense DNA primer with a stop codon and BamHI site

<400> 32  
 cgcggatcct cattctgaac ccagtatact 30

<210> 33  
<211> 9  
<212> PRT  
<213> artificial sequence

<220>  
<223> a mutated ephrin B2 extracellular domain peptide motif

<400> 33

Met Asn Gln Glu Gln Val Ser Pro Leu  
1 5